MULTIMEDIA UNIVERSITY

STUDENT ID NO

MULTIMEDIA UNIVERSITY

FINAL EXAMINATION

TRIMESTER 2, 2018/2019

HPB2011 – BIOINFORMATICS PROGRAMMING I

(All sections / Groups)

6 MARCH 2019
2:30 to 4:30 PM
(2 Hours)

INSTRUCTIONS TO STUDENTS

1. This question paper consists of 6 pages including cover page and 4 questions only.

2. Attempt all **FOUR** questions. All questions carry equal marks (10), and the distribution of the marks for each question is given.

3. Please write all your answers in the Answer Booklet provided

QUESTION 1 [10 marks]

a. NCBI is one of the biological databases, which have both primary and secondary characteristics. Describe briefly the aspects of primary and secondary characteristics, and give an example of NCBI database for each characteristic. [2 marks]

b. Using the dynamic programming method, construct the global alignment score table for the following two sequences and find the possible alignment. The scoring parameters are:
Match score = +1, mismatch score = -1, gap penalty = -1 [4 marks]
CTGTTCC

ATGTTC

c. Briefly describe the protein primary, secondary, tertiary, and quaternary structure.

[4 marks]

QUESTION 2 [10 marks]

What is the output of the following JAVA codes?

i. [1 mark]

```
public class Demo {
 private String[] userNames;

 public Demo() {
  userNames = new String[10];
   }

 public void setName(String s, int n) {
  userNames[n] = s;
 }

 public void showName(int n) {
  System.out.println("Name is " + userNames[n]);
 }

 public String getName(int n) {
  return userNames[n];
 }

 public static void main(String[] s) {
  Demo demo = new Demo();
  demo.showName(2);
 }}
```

Continued...

ii. [1 mark]

```
public class MainClass {
 public static void main(String[] argv) throws Exception {
  System.out.println(testAns("YES", 6));
 }

 public static boolean testAns(String ans, int n) {
  boolean rslt = false;
  if (ans.equalsIgnoreCase("yes") && n > 5)
   rslt = true;
  return rslt;
 }}
```

iii. [1 mark]

```
public class Test {
public static void main(String[] args) {
int[] x = new int[5];
int i;
for (i = 0; i < x.length; i++)
x[i] = i;
System.out.println(x[i]);
}
}
```

iv. [1 mark]

```
public class Test {
   public static void main(String[] args) {
      for(int i = 0;;i++) {
         System.out.println("Hello");
         if (i==2)
         break;
      }
   }
}
```

v. [1 mark]

```
public class Test {
public static void main(String[] args) {
int n = 2;
xMethod(n);

System.out.println("n is " + n);
}

void xMethod(int n) {
n++;
}
}
```

vi. [2 marks]

```
public class RuntimePolymorphism
{
   public static void main(String[] args)
```

```
    {
      A a = new B();
      B b = new B();

      System.out.println(a.c + " " + a.getValue()
        + " " + b.getValue() + " " + b.getSuperValue());
    }
  }
  class A
  {
    protected char c = 'A';
    char getValue()
    {
      return c;
    }
  }
  class B extends A
  {
    protected char c = 'B';
    char getValue()
    {
      return c;
    }
    char getSuperValue()
    {
      return super.c;
    }
  }
```

vii. [1 mark]

```
  public class Test
  {
    public static void main(String[] args)
    {
      int value = 3, sum = 6 + -- value;

      int data = --value + ++value / sum++ * value++ + ++sum  % value--;
      System.out.println(data);
    }
  }
```

viii. [1 mark]

```
  public class comma_operator
  {
     public static void main(String args[])
     {
          int sum = 0;
          for (int i = 0, j = 0; i < 5 & j < 5; ++i, j = i + 1)
               sum += i;
          System.out.println(sum);
     }
  }
```

Continued...

ix. [1 mark]

```
class Alpha
{
  public String type = "a ";
  public Alpha() { System.out.print("alpha "); }
}
public class Beta extends Alpha
{
  public Beta() { System.out.print("beta "); }
  void go()
  {
    type = "b ";
    System.out.print(this.type + super.type);
  }
  public static void main(String[] args)
  {
    new Beta().go();
  } }
```

QUESTION 3 [10 marks]

a. Create a JAVA method count(String sequence) . This method counts the number of 'A', 'C', 'T' and 'G' in the String sequence, which is a parameter to the count function. The function discards any unknown base other than A, C, G, or T .It prints the results as following output:

"Number of A = " ...." C = " ..... " G= "....." T="....." [4 marks]

b. Write correct Java code to

i. Get the path and name of a FASTA file from the user (command line)

ii. Open the file using "try ... catch"

iii. Create a "FASTAobject" object from the class Fasta.

iv. Read information from the FASTA file, one line at a time, and store it in the correct attribute in the FASTAobject. To parse the first line into accession number and "description" you might need String methods "indexOf(...)" and "substring(...)"

v. Close the FASTA file when you are finished [6 marks]

Continued...

QUESTION 4 [10 MARKS]

a. Write a java interface "Human" which contains a String attribute name (you have to initiate the attribute to anyname). The interface has two functions speak() which returns nothing, and getName() which returns the name of the human. Write a class called Malaysian and uses the interface Human. The Malaysian class has an attribute province. Complete the class Malaysians with required functions.

[3 marks]

b. The following table is an excerpt from a substitution matrix; note that the characters in the top row and first column can be treated as integers (char). Write a Java method to take 2 input Strings and the table – public void scoreTbl(String seqA, String seqB, int[][] tbl). It: [7 marks]

	C	T	P	A
C	12	-2	-3	-2
S	0	1	1	1
T	-2	3	0	1
P	-3	0	6	1
A	-2	1	1	2

i. finds the minimum length between seqA and seqB (which one is shorter)

ii. loops through seqA (up to minimum length), gets each char, searches the first column in tbl for that char

iii. gets corresponding char in seqB, searches the top row in tbl for that char.

iv. gets the value in tbl[rowA][colB] and adds it to the total score for the sequence match

v. at the end displays the total score.

END OF PAPER